Sub C2

B9

21. Use of a nucleic acid according to Claim 1, of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to Claim 13, or of a pharmaceutical composition according to Claim 19 for preparing an agent for exerting an effect on the binding of fibrinogen to blood platelets.

B10

25. Process according to Claim 23, characterized in that the antibody-encoding nucleic acids are used for expressing recombinant antibody chains, or derivatives or fragments thereof.

REMARKS

In accordance with 37 C.F.R. 1.821(C), Applicants submit herewith the Sequence Listing for the above-identified application both in paper copy form and in computer readable form.

The name of the file on the computer readable form is 05649049.APP. The paper copy and the computer readable copy are the same.

Claims 1-25 are currently pending. In response to the Examiner's request made during a telephone interview on April 18, 2001, claims 3, 6, 11, 12, 13, 16, 17, 19, 20, 21 and 25 are amended herein to eliminate multiple dependencies. Claims 1-25, as amended, are presented for reconsideration.

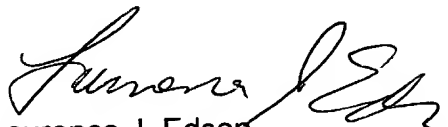
In view of the amendments and remarks above, Applicants submit that this application is in condition for examination on the merits and request consideration and favorable action thereon.

If for any reason, the Examiner feels the application is not now in condition for examination, it is respectfully requested that the Examiner contact, by telephone, Applicants' undersigned attorney at the indicated telephone number to arrange for an interview to expedite the disposition of this application.

In the event this paper is not considered to be timely filed, Applicants hereby petition for an appropriate extension of time. The fee for this extension may be charged to our Deposit Account No. 01-2300, along with any other fees which may be required with respect to this paper.

Respectfully submitted,

ARENT FOX KINTNER PLOTKIN & KAHN, PLLC



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Enclosures: Marked-Up Copy of Claims
Substitute Tables 3, 6, 7a and 7b
Petition for Extension of Time
Sequence Listing

#28633-1

MARKED-UP CLAIMS

3. (Twice Amended) Nucleic acid according to [either] Claim 1 [or 2], which furthermore comprises a CDR2 region, selected from:

(a) a nucleotide sequence which encodes the amino acid sequence:

D I S Y S G S T K Y K P S L R S, (SEQ ID NO:35)

(b) a nucleotide sequence which encodes the amino acid sequence:

V I S Y D G S N K Y Y A D S V K G, (SEQ ID NO:36)

and

(c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).

6. (Twice Amended) Nucleic acid according to Claim 4 [or 5], which furthermore comprises a CDR2 region selected from:

(a) a nucleotide sequence which encodes the amino acid sequence:

G S H Q R P S, (SEQ ID NO:41)

(b) a nucleotide sequence which encodes the amino acid sequence:

S N N Q R P S, (SEQ ID NO:42)

and

(c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).

11. Vector, characterized in that it

(a) contains at least one copy of a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or at least one copy of a nucleic acid according to [one of Claims] Claim 4 [to 6] or

(b) contains at least one copy of a nucleic acid according to Claim 7 [or 8] and/or at least one copy of a nucleic acid according to [Claims] Claim 9 [or 10].

12. Cell, characterized in that it

(a) expresses a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or a nucleic acid according to [one of Claims] Claim 4 [to 6] or

(b) a nucleic acid according to Claim 7 [or 8] and/or a nucleic acid according to Claim 9 [or 10].

13. Polypeptide, characterized in that it

(a) is encoded by a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or a nucleic acid according to [one of Claims] Claim 4 [to 8] or

(b) by a nucleic acid according to Claim 7 [or 8] and/or a nucleic acid according to Claim 9 [or 10].

16. Polypeptide according to [one of Claims] Claim 13 [to 15], characterized in that it is coupled to a labelling group or a toxin.

17. Antibody against a polypeptide according to [one of Claims] Claim 13 [to 16].

19. Pharmaceutical composition which comprises, as the active component, a nucleic acid according to [one of Claims] Claim 1 [to 10], a vector according to Claim 11, a cell according to Claim 12, a polypeptide according to [one of Claims] Claim 13 [to 16] or an antibody according to [either] Claim 17 [or 18], where appropriate together with other active components and pharmaceutically customary adjuvants, additives or excipients.

20. Use of a nucleic acid according to [one of Claims] Claim 1 [to 10], of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to [one of Claims] Claim 13 [to 16], of an antibody according to Claim 17 [or 18], or of a pharmaceutical composition according to Claim 19 for preparing an agent for the diagnosis or for the treatment or prevention of AITP.

21. Use of a nucleic acid according to [one of Claims] Claim 1 [to 10], of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to [one of Claims] Claim 13 [to 16], or of a pharmaceutical composition according to Claim 19 for preparing an agent for exerting an effect on the binding of fibrinogen to blood platelets.

25. Process according to Claim 23 [or 24], characterized in that the antibody-encoding nucleic acids are used for expressing recombinant antibody chains, or derivatives or fragments thereof.

Table 3

A. Heavy Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
VH4.11		QVQLQESGPGLVKPSETLSLTCTVSGGSIS		SYYWS		WIRQPPGKGLEWIG		YIYYSGSTNYNPSLKS		RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR				
PDG7	2	--K-L----------N-----R---		G-S-R		----S---------		D-S-----K-K---R-		---L----------N----------		VLPFDPISMDV		WGKGTTVTVSS
PDG8		----------		-----		----------		----------		----------		VLPFDPISMDV		WGKGTTVTVSS
PDG10		----------		-----		----------		----------N---		----------		VLPFDPISMDV		WGKGTTVTVSS
PDG16		----------		-----		----------		----------N---		----------		VLPFDPISMDV		WGKGTTVTVSS
1.9III		QVQLVESGGGVVQPGRSLRLSCAASGFTES		SYGMH		WVRQAPGKGLEWVA		VISYDGSNKYYADSVKG		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK				
PDG13	6	--K-L----------		--A--		----------		----------		--A----------R		ALGSWGGWDHYMDV		WGKGTTVTVSS
PDG17		----------		-----		----------		----------		----------		ALGSWGGWDHYMDV		WGKGTTVTVSS
PDG31		----------		-----		----------		----------N----		----------		ALGSWGGWDHYMDV		WGKGTTVTVSS
PDG37		----------		-----		----------		----------N----		----------		ALGSWGGWDHYMDV		WGKGTTVTVSS
H85255		----------		-----		----------		----------N----		----------		DRPIARWTYGGMDV		WGQGTTVTVSS

B. Light Chains

Clones	SEQ ID	FR1	ID	CDR1	ID	FR2	ID	CDR2	ID	FR3	ID	CDR3	ID	FR4
DPL2		VLTQPPSASGTPGQRVTISC		SGSSSNIGSNTVH		WYQQLPGTAPKLLIY		SNNQRPS		GVPDRFSGSKSGTSASLAISGLQSEDEADYYC		AAWDDSLNG		
PDG7	4	-V----------W-----		-------R--P-S		--H-V---------F		GSH----		----------R----G-AG----		-T---G---PV		FGGGTKLTVLSQP
PDG8		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP
PDG10		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP
PDG16		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP
DPL2		VLTQPPSASGTPGQRVTISC		SGSSSNIGSNTVN		WYQQLPGTAPKLLIY		SNNQRPS		GVPDRFSGSKSGTSASLAISGLQSEDEADYYC		AAWDDSLNG		
PDG13	8	-V----------		----------		----------		-------		----------		---------WV		FGGGTKLTVLSQP
PDG17		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP
PDG31		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP
PDG37		----------		----------		----------		-------		----------		----------		FGGGTKLTVLSQP

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (VH4.11; 1.9III; DPL2) are given for comparative purposes and in each case represent the deduced amino acid sequence for the most closely related published strainline gene sequence. Dashes denote identity. M85255 refers to the EMPL/GenBank reference number and denotes the deduced amino acid sequence of the human anti-GPIIb autoantibody 2E7 (Kunicki et al., J. Autoimmun. 4 (1991), 433-446). In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of PDG7 and PDG13 are presented in SEQ ID NO:2 and 6, respectively. The amino acid sequences of the light chains of PDG7 and PDG13 are presented in SEQ ID NO:4 and 8, respectively.

Table 6

anti-Id phage clones antiidiotypic phab clones (AI-X and AI-B)	H Chain				L Chain			
	Seq. ID No(s).	V_H family	Straightline Gene	Homology (%)*	Seq. ID No(s).	V_λ family	Strainline gene	Homology (%)*
AI-X16	10, 54, 74, 75, 43	V_H3	DP47	88	12, 80, 81	$V_\lambda2$	DPL10	88
AI-X24	-	V_H3	DP47	88	-	$V_\lambda2$	DPL10	88
AI-X17	76	V_H3	DP47	87	-	$V_\lambda2$	DPL10	88
AI-X39	16, 55, 77, 44	V_H3	DP49	94	-	-	-	-
AI-X40	123, 56, 78, 45	V_H3	DP31	95	-	-	-	-
AI-X20	14, 57, 79, 46	V_H4	DP71	78	-	-	-	-
AI-B14	22, 83, 84, 85	V_H3	DP46	91	-	-	-	-
AI-B17	-	V_H3	DP46	91	-	-	-	-
AI-B18	24, 86, 87, 88	V_H1	DP10	85	-	-	-	-
AI-B24	26, 127, 88, 89	V_H3	DP49	81	122, 116, 99	$V_\lambda3$	3h	82
AI-B38	30, 94, 98, 90	V_H1	DP5	98	-	-	-	-

* Highest homology (in %) of the amino acid sequences of the respective phab clones with sequences of known strainline V genes

Table 7a

A. Heavy Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
DP47		EVQLLESGGGLVQPGGSLRLSCAASGFTFS	103	SYAMS		WVRQAPGKGLEWVS	107	AISGSGGSTYYADSVKG		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK				
AIX16	10	Q-K---------H----------D	54	NF---		----------	74	G---G-LL-H-------	75	------N--R--V----------	43	VRDLGYRVLSTFTFDI		WGQGTKVTVSS
AIX24		----------		-----		----------		----------		----------		----------		----------
AIX17		----------r-		-----		----------	76	----------N----		----------		----------		----------
DP49		QVQLVESGGGVVQPGRSLRLSCAASGFTFS	104	SYGMH		WVRQAPGKGLEWVA	108	VISYDGSNKYYADSVKG		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK				
AIX39	16	--K-L-------H----------	55	--T--		----------	77	L----------		--A----------K----------	44	DGRSGSYARFDGMDV		WGQGTTVTVSS
DP31		EVQLVESGGGLVQPGRSLRLSCAASGFTFD	105	DYAMH		WVRQAPGKGLEWVS	109	GISWNSGSIGYADSVKG		RFTISRDNAKNSLYLQMNSLRAEDTALYYCAKD				
AIX40	123	--K-L----------	56	---L-		----------	78	----D-T----------		----------V--	45	MGSSVVATYNAFDI		WGQGTMVTVSS
DP71		QVQLQESGPGLVKPSETLSLTCTVSGGSIS	106	SYYWS		WIRQPPGKGLEWIG	110	YIYYSGSTNYNPSLKS		RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR				
AIX20	14	--K-L----------DV--R	57	-H---		-L----------	79	F--DGAR-RF----R-		--SL-M-P-K-------G------S-------	46	DADGDGFSPYYFPY		WGQGIPVSVSS

B. Light Chains

Clones	SEQ ID	FR1	ID	CDR1	ID	FR2	ID	CDR2	ID	FR3	ID	CDR3	ID	FR4
DPL10		QSALTQPASVSGSPGQSITISC	124	TGTSSDVGSYNLVS		WYQQHPGKAPKLMIY	125	EVSKRPS		GVSNRFSGSKSGNTASLTISGLQAEDEADYYC	126	CSYAGSSTF		
AIX16	12	VV----------	80	-----AI-N--F-P		----------	81	-G-----		----------E---	82	---VH---N		WVFGGGTKLTVLGQPKAAPSVTLFPPSS
AIX24		----------		----------		----------		-------		----------		---------		----------
AIX17		----------		----------		----------		-------		----------		---------		----------

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (DP47, DP49, DP31, DP71 and DPL10) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of AIX16, AIX39, AIX40, and AIX20 are presented in SEQ ID NO:10, 16, 123 and 14, respectively. The amino acid sequences of the CDR1 regions of the heavy chains of AIX16, AIX39, AIX40, AIX20, DP47, DP49, DP31 and DP71 are presented in SEQ ID NO:54, 55, 56, 57, 103, 104, 105 and 106, respectively. The amino acid sequences of the CDR2 regions of the heavy chains of AIX16, AIX17, AIX39, AIX40, AIX20, DP47, DP49, DP31 and DP71 are presented in SEQ ID NO:74, 76, 77, 78, 79, 107, 108, 109 and 110, respectively. The amino acid sequence of the light chain of AIX16 is presented in SEQ ID NO:12. The amino acid sequences of the DCR1, CDR2 and CDR3 regions of AIX16 are presented in SEQ ID NO:80, 81, and 82, respectively. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of DPL10 are presented in SEQ ID NO:124, 125 and 126, respectively.

Table 7B

A. Heavy Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
DP46		QVQLVESGGGVVQPGRSLRLSCAASGFTFS	91	SYAMH	95	WVRQAPGKGLEWVA		VISYDGSNKYYADSVKG		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR				
AI-B14	22	--K-L--------------------------	83	D-G--	84	--------------		A----------------		--S------N-------ST---------F---	85	DSETAIAAAGRFDI		WGQGTMVTVSS
AI-B17		------------------------------		-----		--------------		----------------		-------------------------------		--------------		----------
DP-10		QVQLVQSGAEVKKPGSSVKVSCKASGGTFS	92	SYAIS	96	WVRQAPGQGLEWMG		GIIPIFGTANYAQKFQG		RVTITADESTSTAYMELSSLRSEDTAVYYCAR				
AI-B18	24	--K-LE-----------M----------	86	-HT--	87	--------------		--T-----V--------		--------P--------R--T-DDSGI-----	88	EDGTTVPSQPLEF		WGQGTRVTVSS
DP-49		QVQLVESGGGVVQPGRSLRLSCAASGFTFS	93	SYGMH	97	WVRQAPGKGLEWVA		VISYDGSNKYYADSVKG		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK				
AI-B24	26	--K-L-----L----G------S------N	127	K-AI-	88	----------Y-S		A--SN-G-T--------		----------V----S----------VR	89	GSGSYLGYYFDY		WGQGTLVTVSS
DP-5		QVQLVQSGAEVKKPGASVKVSCKVSGYTLT	94	ELSMH		WVRQAPGKGLEWMG		GFDPEDGETIYAQKFQG		RVTMTEDTSTDTAYMELSSLRSEDTAVYYCAT				
AI-B38	30	Q-K-LE------------------------	94	-----	98	--------------		----------------		-------------------------------	90	GLRSYNYGRNLDY		WGQGTLVTVSS

B. Light Chains

Clones	SEQ ID	FR1	ID	CDR1	ID	FR2	ID	CDR2	ID	FR3	ID	CDR3	ID	FR4
VL3h		SYVLTQPPSVSVAPGKTARITC	100	GGNNIGSKSVH		WYQQKPGQAPVLVIT	101	YDSDRPS		FIPERFSGSNSGNTATLTISRVEAGDEADYYC	102	QVWSSSSDH		
AI-B24		-V----------RQ--T---	122	--YK-------		----------V-	116	E--Y---		E----------M-----TG----------	99	----NTN-Q		TIFGGGTKLTVLRQPKAAPSVTLFPPSS

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (DP46, DP10, DP49, DP5 and VL3h) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of A-B14, AI-B18, AI-B24 and AI-B38 are presented in SEQ ID NO:22, 24, 26 and 30, respectively. The amino acid sequences of the CDR1 regions of the heavy chains of AI-B14, AI-B18, AI-B24, AI-B38, DP-46, DP-10, DP-49 and DP-5 are presented in SEQ ID NO:83, 86, 127, 94, 91, 92, 93 and 94, respectively. The amino acid sequences of the CDR2 regions of the heavy chains of AI-B14, AI-B18, AI-B24, AI-B38, DP-46, DP-10, DP-49 and DP-5 are presented in SEQ ID NO:84, 87, 88, 98, 95, 96, 97 and 98, respectively. The amino acid sequence of CDR3 regions of the heavy chains of AI-B14, AI-B18, AI-B24, and AI-B38 are presented in SEQ ID NO:85, 88, 89 and 90, respectively. The amino acid sequences of the light chain of AI-B24 is presented in SEQ ID NO:28. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of the light chains of AI-B24 are presented in SEQ ID NO:122, 116 and 99, respectively. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of the light chains of VL3h are presented in SEQ ID NO:100, 101 and 102, respectively.